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CONTENTS/SUMMARIES

Summary: Bacteria contain several small proteins which share some biochemical properties with eucaryotic histones. The prototype histonelike protein is called HU, a small, basic, abundant, deoxyribonucleic acid (DNA)-binding protein whose amino acid sequence is conserved among many bacteria and is homologous with sequences of similar proteins obtained from chloroplasts and archaebacteria. When purified HU binds to DNA, it appears to wrap the DNA into nucleosomelike structures in which negative supercoils are constrained. Recently HU has been found to affect site-specific interactions of other proteins with DNA, acting as a positive or a negative effector depending on the system. IHF, the host factor involved in the integration of bacteriophage lambda into the host chromosome, can also be considered histonelike on the basis of amino acid sequence homologies with HU. IHF is involved in wrapping DNA, and it participates in a variety of site-specific interactions of proteins with DNA. The biochemical properties of HU and IHF, as well as of three other proteins, H, H1, and FirA, are reviewed in the context of possible participation in bacterial chromatin structure and site-specific interactions of protein with DNA.

Summary: The free energy of some decarboxylation reactions can be conserved by conversion into an electrochemical gradient of Na^+ ions. This new type of biological energy conservation was detected during studies of oxaloacetate decarboxylase of Klebsiella pneumoniae. *Other sodium ion-pumping decarboxylases include methylmalonyl-coenzyme A decarboxylase and glutaconyl-coenzyme A decarboxylase. These enzymes occur in anaerobic bacteria, where they catalyze an essential reaction of the fermentation pathway and thereby conserve energy. These energy-transducing decarboxylases have been purified; the composition of subunits and details of their catalytic mechanism has been investigated. The Na^+ transporting capacity of the purified enzymes was established by reconstituting them into proteoliposomes. These three decarboxylases are closely related with respect to structure and function. Another primary Na^+ pump found in bacteria is the respiratory Na^+ pump of* Vibrio alginolyticus. *A variety of other functions of Na^+ ions in bacteria are known. Solute transport systems coupled to Na^+ ion gradients occur in many bacteria. In alkalophilic bacteria, an Na^+/H^+ antiporter is of central importance for pH homeostasis. Motion of the flagella of some alkalophilic or marine bacteria is powered by an electrochemical Na^+ gradient. The strict anaerobe* Propionigenium modestum *synthesizes adenosine triphos-*

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phate exclusively by energetic coupling to the electrochemical Na^+ gradient established by methylmalonyl-coenzyme A decarboxylase. This is the first example of adenosine triphosphate synthesis coupled to the free energy of a decarboxylation reaction; it is also the first example of an adenosine triphosphate synthesis mechanism with Na^+ as coupling ions.

Summary: While the action of many antibiotics, with a single key step, is well understood, the highly pleiotropic effects of the aminoglycosides resisted coherent explanation until the recent proposal that misread proteins are incorporated into the cytoplasmic membrane, fit poorly, and create aqueous channels. In the resulting multistep model, several effects are equally essential for bactericidal action: misreading on chain-elongating ribosomes, incorporation of misread protein in the membrane, resulting formation of channels, entry of more antibiotic, and irreversible blockade of the initiating ribosomes. The ability of this model to account for many additional features of aminoglycoside action is reviewed in some detail. The reasons for the long neglect of the membrane damage, demonstrated 25 years ago, are also discussed. In light of this mechanism, earlier observations on the effect of puromycin lead to the further conclusion that the products of premature chain termination, even without misreading, also can cause membrane damage.

Summary: The metal-regulated genetic system of yeast metallothionein (MT) provides an excellent opportunity for the geneticist, the pharmacologist, and the inorganic chemist to study various aspects of metal metabolism. MT binds several transition metals, and the structure of MT is guided by the metal bound. In naturally occurring or laboratory Saccharomyces cerevisiae *strains, the resistance to copper is directly related to the number of chromosomal MT genes. The MT gene system of* S. cerevisiae *is an excellent model system to study mechanism of drug resistance via gene amplification. Yeast MT gene transcription is efficiently regulated by copper. Regulation of the yeast MT gene by copper has provided a powerful tool for expression of heterologous genes in yeasts. A model describing mechanisms of MT gene regulation in yeast cells has been proposed. The availability of several* S. cerevisiae *strains with well-defined MT genetic markers offers opportunities for coamplification of foreign genes on chromosomal MT loci. Several applications of yeast MT in research and metal recovery are discussed.*

Summary: The existence of a viable but nonculturable stage in which bacterial cells are intact and alive when tested by one or more criteria but do not undergo cell division in or on routinely employed bacteriological media has been observed for many aquatic and marine bacteria. Because this phenomenon has recently attracted considerable attention, the observations reported during the past two decades relating to the viable but nonculturable state have been reviewed, and the findings are presented here. Nutrient transport and permeability appear to be important for maintaining viability of bacteria. In early stages of nutrient limitation, adaptation is critical and can be very different depending upon the bacterial species, recent nutrient history of the population involved, trophic status, tolerance level for the environmental change encountered, nature and extent of the alteration, and interactive effects thereof. Clearly what may be a large adjustment for one population may be minor for another. The decline period in bacterial growth, observed in response to some adverse condition by culture methods of enumeration, may in fact represent the survival period. The first phase of the survival period includes loss of culturability or temporary cessation of cell replication as a means of conservation of energy. Cessation may be easily reversed in the second phase

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by simple procedures permitting acclimation to the new conditions, in which case reversion to culturability is observed. Prolonged exposure to the changed conditions may result in an inability to induce reversion of the loss of replication while other cell activities continue. This, the third phase, can be characterized by uptake of labeled substrates and demonstration of viability by cell elongation in the direct viable counting procedure, employing microscopic observation. Further exposure to adverse conditions may result in cessation of response in the direct viable counting procedure but continued activity as measured by labeled substrate uptake, representing phase four. Phase five may ensue if exposure to adversity continues beyond that inducing phase four; the response is slowed metabolic activity, to the point where uptake is low enough to be below the threshold level required for detection by activity measurement methods. Cells remain intact and retain their integrity when viewed by epifluorescence microscopy. Cells may be dormant in this phase. Upon losing cellular integrity and without activity being observed, the population of bacterial cells is considered dead, the final phase. We propose a continuum of events with the sequential phases, or stages, able to be characterized employing currently available methods. We propose that at any phase in the survival period reversion may occur by provision of the proper conditions, thereby providing for cyclical survival response. Unfortunately, the proper conditions are not yet known for all bacterial species undergoing the somnicell stages of development.

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